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International Workshop "Algorithmics, Bioinformatics and Statistics for NGS data analysis" - June 22-23 2015

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[-> https://sites.google.com/site/abs4ngs/workshop2015]

In the last years, high-throughput sequencing technologies (NGS: Next-Generation Sequencing) became a dominant tool in almost all kinds of genomics studies: gene expression, copy number variation, methylation, protein-DNA and DNA-DNA interactions, and many others biological questions. The Workshop, organized by ABS4NGS project, will bring together scientists working in biology, bioinformatics, computer science and statistics in order to present and discuss recent advancements in the analysis of NGS data. A non-exhaustive list of topics includes genome sequencing and reconstruction, analysis of transcriptional landscape, models of epigenomics, and other computational and statistical tools recently proposed by the research community.

Scope

The workshop will cover both methodological issues of NGS data analysis and biological questions that can be answered through the analysis of high throughput sequencing datasets. Planned invited speakers include computational scientists, bioinformaticians, molecular biologists and clinicians working with NGS data. Workshop topics will include:

- Methodology of read mapping, assembly and automatic strategies for read error correction,
- Variant calling and clinical applications of NGS,
- High Throughput Chromosome Conformation Capture analysis, domain detection and inferring the three-dimensional structure of the genome,
- Transcriptome assembly, isoform quantification and annotation of abnormal transcripts in cancer datasets,
- Strategies for ChIP-seq data analysis and their application for prediction of epigenetic regulation.